AMENDMENTS TO THE CLAIMS

1. (withdrawn) A modified cytochrome P450 monooxygenase which, in comparison with the wild-type enzyme, shows an altered substrate profile in the terminal and/or subterminal enzymatic hydroxylation of aliphatic carboxylic acids, owing to site-specific mutagenesis of its substrate binding region.

2. (withdrawn) A monooxygenase as claimed in claim 1, which is derived from cytochrome P450 monooxygenases of bacterial origin.

3. (withdrawn) A monooxygenase as claimed in claim 2, which is derived from Bacillus megaterium cytochrome P450 monooxygenase BM-3 with an amino acid sequence in accordance with SEQ ID NO: 2, which has at least one functional mutation in one of the following amino acid sequence regions: 24-28, 45-51, 70-72, 73-82, 86-88, 172-224 and 352-356, with the proviso that, if the enzyme carries the mutation F87A, more than one of these regions is mutated.

4. (withdrawn) A monooxygenase as claimed in claim 3, which comprises at least one functional mutation in the amino acid sequence regions 86-88 and 172-224.

5. (withdrawn) A monooxygenase as claimed in claim 4, which comprises at least one of the following amino acid substitution patterns:

   a) F87V;

   b) F87A L188K;

   c) F87V L188K;

   d) F87A L188K A74G;

   e) F87V L188K A74G;

   f) F87A L188K A74G R47F;

g) F87V L188K A74G R47F;

h) F87A L188K A74G R47F V26T; or

i) F87V L188K A74G R47F V26T;

and functional equivalents thereof.

6. (withdrawn) A monooxygenase as claimed in claim 3, which comprises a single amino acid substitution from amongst the following:

a) V26T,

b) R47F,

c) S72G,

d) A74G,

e) F87V,

f) L188z, where Z is an amino acid selected from amongst K, R, W, Q, N, G, A and S, and

g) M354T;

and functional equivalents thereof.

7. (withdrawn) A nucleic acid sequence encoding a monooxygenase as claimed in claim 1 and the complementary nucleic acid sequence thereof.

8. (withdrawn) An expression construct comprising, under the genetic control of regulatory acid sequence, an encoding sequence which encompasses a nucleic acid sequence as claimed in claim 7.

9. (withdrawn) A vector which encompasses at least one expression construct as claimed in claim 8.

10. (withdrawn) A recombinant microorganism which has been transformed with at least one

vector as claimed in claim 9.

11. (withdrawn) A microorganism as claimed in claim 10, selected from amongst bacteria of the genus Escherichia.

12. (currently amended) A process for the enzymatic production of subterminally hydroxylated aliphatic carboxylic acids, which comprises

a1) culturing a recombinant microoganism which has been transformed with a vector which encompasses an expression construct comprising, under the genetic control of regulatory nucleic acid sequences, a sequence which encompasses a nucleic acid sequence encoding a monooxygenase which is derived from *Bacillus megaterium* cytochrome P450 monooxygenase BM-3 with an amino acid sequence in accordance with SEQ ID NO: 2, which has a functional mutation in the amino acid sequence region 86-88 and optionally at least one further functional mutation in one of the following amino acid sequence regions: 24-28, 45-51, 73-82, and 172-224, with the proviso that, if the enzyme carries the mutation F87A, more than one of these regions is mutated, which functional mutation ~~modified cytochrome P450 monooxygenase which~~, in comparison with the wild-type enzyme, ~~shows an altered substrate profile~~ results in an altered activity or regioselectivity in the subterminal enzymatic hydroxylation of ~~aliphatic carboxylic acids, owing to site-specific mutagenesis of its substrate binding region,~~ an aliphatic C_8-C_{12}-carboxylic acid, whereby culturing is performed in the presence of a culture medium which contains at least one hydroxylatable C_8-C_{12}-carboxylic acid or ~~at least one hydroxylatable C_8-C_{12}-carboxylic acid~~ a derivative thereof selected from at alkyl ester, an amide or an anhydride thereof; or

a2) incubating a reaction medium containing at least one hydroxylatable C_8-C_{12}-carboxylic acid or ~~at least one hydroxylatable C_8-C_{12}-carboxylic acid~~ a derivative thereof, selected from an alkyl ester, an amide or an anhydride thereof with ~~said~~ a modified monooxygenase as defined above, and

b) isolating the resulting hydroxylated product from the medium.

13. (canceled)

14. (currently amended) A method as claimed in claim 12, wherein the hydroxylatable carboxylic acid is a C_8-C_{12}-monocarboxylic acid or a derivative thereof and the monooxygenase ~~(SEQ ID NO:2) used~~ comprises at least one of the following amino acid substitution patterns in an amino acid sequence according to SEQ ID NO: 2:

a) F87V;

b) F87A and L188K;

c) F87V and L188K;

d) F87A L188K and A74G;

e) F87V L188K and A74G;

f) F87A L188K A74G R47F;

g) F87V L188K A74G R47F;

h) F87A L188K A74G R47F V26T; or

i) F87V L188K A74G R47F V26T.

15. (canceled)

16. (currently amended)A method a claimed in claim 12, wherein the ~~reaction~~ enzymatic production is carried out in the presence of an electron donor or a reduction equivalent.

17. (previously presented) A method as claimed in claim 16, wherein the electron donor or

the reduction equivalent is selected from amongst NADH, NADPH and Zn/CO(III) sepulchrate.

18. (new) The process of claim 12, wherein the monooxygenase comprises at least one functional mutation in the amino acid sequence regions 86-88 and 172-224.